

SEQUENCE LISTING

<110> GRAY, Kevin A.
ABOUSHADI, Nahla
GARRETT, James B.

<120> AMYLASES, NUCLEIC ACIDS ENCODING THEM AND METHODS
FOR MAKING AND USING THEM

<130> 564462003900

<140> US 10/532,944

<141> 2003-10-15

<150> PCT/US03/33150

<151> 2003-10-15

<150> US 60/423,626

<151> 2002-10-31

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Asp Phe Asp Arg Leu Leu Ala Lys Ala His Ala Leu Gly Leu Lys Val
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Trp Ala Asp Pro Arg Glu Asp Gly Thr Pro Pro Asn Asn Trp Met Ser
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Ile Phe Gly Gly Val Ala Trp Gln Trp Glu Pro Arg Arg Glu Gln Tyr
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Tyr Asn Asn Thr Gln Pro Glu Asn Ile Gly Phe Ile Glu Arg Leu Arg
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Ala Glu Asp Ser Leu Ala Thr Thr Ala Glu Tyr Thr Ala Pro Gly Arg
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Gly Tyr Ile Arg Asp Thr Val Ser Arg Leu Glu Ala Thr Met Thr Glu
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Gly Trp Pro Cys Trp Ala Ile Ser Asn His Asp Val Glu Arg Ala Val
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Thr Arg Trp Gly Gly His Pro Ala Arg Pro Arg Leu Ala Arg Met Leu
370          375          380
Val Ala Leu Leu Cys Ser Leu Arg Gly Ser Ile Cys Leu Tyr Gln Gly
385          390          395          400
Glu Glu Leu Gly Leu Gly Glu Ala Asp Val Pro Phe Glu Ala Leu Gln
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Asp Pro Tyr Gly Ile Thr Phe Trp Pro Asn Phe Lys Gly Arg Asp Gly
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Cys Arg Thr Pro Met Pro Trp Ile Asp Ala Pro Leu Ala Gly Phe Thr
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 Ile Val Phe Leu Gln Thr Ala Glu Pro Val Leu Met Phe Glu Arg Arg
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 His Ala Gly Glu Thr Leu Leu Leu Ala Phe Asn Leu Ala Ala Asp Thr
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 Ala Arg Val Ala Leu Pro Ala Gly Ser Trp Gln Pro Met His Val Pro
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 <212> DNA
 <213> Unknown

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 <223> Obtained from an environmental sample

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 35 40 45
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Glu Trp Arg Thr Val Arg Asn His Tyr Asn Glu Leu Ala Ile Thr Phe
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Glu Glu Lys Thr Lys Leu His Arg Arg Met Arg Ile Val Phe Arg Leu
115 120 125
Phe Asp Glu Gly Ile Gly Phe Arg Tyr Glu Leu Pro Arg Gln Pro Asn
130 135 140
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Arg Pro Gly Thr Ala Trp Trp Ala Pro Ala Phe Glu Ser Asn Arg Glu
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Glu Tyr Leu Tyr Asn Gln Thr Pro Ile Asp Gly Val Ala Ile Ala Met
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Thr Pro Phe Thr Met Arg Phe Glu Asp Gly Thr His Leu Ser Ile His
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Glu Ala Ala Leu Val Asp Tyr Ser Gly Met Asn Val Thr Arg Val Gln
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Gly Thr Asn Phe Lys Ala Ile Leu Thr Pro Gly Ser Met Gly Pro Lys
225 230 235 240
Val Ser Arg Asp Thr Pro Phe Glu Thr Pro Trp Arg Val Ile Leu Ile
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260 265 270
Leu Asn Glu Pro Asn Lys Leu Gly Asp Val Ser Trp Val His Pro Arg
275 280 285
Lys Tyr Val Gly Ile Trp Trp Gly Met His Leu Asp Thr Gln Ser Trp
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Ala Ser Gly Pro Lys His Gly Ala Thr Thr Ala Tyr Ala Lys Arg Met
305 310 315 320
Ile Asp Phe Ala Ala Thr Asn Gly Phe Thr Gly Leu Leu Val Glu Gly
325 330 335
Trp Asn Lys Gly Trp Asp Gly Asp Trp Phe Ala Thr Gly Asp Asp Phe
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Ser Phe Thr Glu Pro Tyr Pro Asp Phe Asp Ile Arg Ala Val Ala Ala
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Tyr Ser Leu Arg Lys Gly Val His Leu Ile Gly His His Glu Thr Ser
370 375 380
Gly Asn Ile Ala His Tyr Glu Gln Gln Leu Asp Ala Ala Leu Asp Leu
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<210> 8
 <211> 781
 <212> PRT
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Arg Pro Ser Arg Phe Asp Val Asp His Asp Gly Trp Ala Thr Val Gln
          35          40          45
Tyr Asp Ala Gly Val Met Val Gly Val Ala Ala Leu Asp Asp Thr Val
          50          55          60
Leu Arg Val Ala Tyr Cys Arg Ser Pro Gly Glu Trp Pro Thr Ser Thr
65          70          75          80
Pro Ala Ile Val Glu Gln Met Ser Gln Arg His Ser Trp Arg Leu Val
          85          90          95
Gln Glu Glu Arg Arg Val Gln Leu Glu Cys Val Ala Gly Trp Gln Ile
          100          105          110
Gln Ile Asn Arg Asp Asp Gly Thr Trp Ser Ile Arg His Leu Gly Phe
          115          120          125
Gly Thr Ala Val Glu Ala Ile Thr Trp Tyr Lys Arg Lys Lys Gly Gly
          130          135          140
Ala Leu Thr Phe Ala Ser Leu Asp Asn Ala Arg Phe Tyr Gly Leu Gly
145          150          155          160
Glu Lys Pro Gly Pro Leu Asp Lys Arg His Glu Ala Tyr Thr Met Trp
          165          170          175
Asn Ser Asp Val Tyr Ala Pro His Val Pro Glu Met Glu Ala Leu Tyr
          180          185          190
Leu Ser Ile Pro Phe Phe Leu Arg Leu Gln Asp Gln Thr Ala Val Gly
          195          200          205
Ile Phe Val Asp Asn Pro Gly Arg Ser Arg Phe Asp Phe Arg Ser Arg
210          215          220
Tyr Pro Asp Val Glu Ile Ser Thr Glu Arg Gly Gly Leu Asp Val Tyr
225          230          235          240
Phe Ile Phe Gly Ala Ser Leu Lys Asp Val Ile Arg Arg Tyr Thr Lys
          245          250          255

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PC	Leu	Thr	Gly	Arg	Met	Pro	Met	Pro	Pro	Lys	Trp	Ala	Leu	Gly	Tyr	His
			260					265						270		
Gln	Ser	Arg	Tyr	Ser	Tyr	Glu	Thr	Gln	Ser	Glu	Val	Leu	Ser	Val	Ala	
		275					280						285			
Gln	Thr	Phe	Val	Glu	Arg	Asp	Ile	Pro	Val	Asp	Ala	Leu	Tyr	Leu	Asp	
	290					295					300					
Ile	His	Tyr	Met	Asp	Gly	Tyr	Arg	Val	Phe	Thr	Phe	Asp	Glu	Arg	Arg	
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Phe	Pro	Asp	Pro	Ala	Arg	Met	Cys	Asp	Glu	Leu	Arg	Lys	Leu	Gly	Val	
			325						330					335		
Arg	Val	Val	Pro	Ile	Val	Asp	Pro	Gly	Val	Lys	Gln	Asp	Pro	Glu	Tyr	
		340						345					350			
Pro	Val	Tyr	Met	Asp	Gly	Leu	Ala	His	Asn	His	Phe	Cys	Gln	Thr	Ala	
	355						360					365				
Glu	Gly	Gln	Val	Tyr	Leu	Gly	Glu	Val	Trp	Pro	Gly	Leu	Ser	Ala	Phe	
	370					375					380					
Pro	Asp	Phe	Ala	Ser	Glu	Glu	Val	Arg	Ala	Trp	Trp	Gly	Lys	Trp	His	
385					390					395					400	
Arg	Val	Tyr	Thr	Gln	Met	Gly	Ile	Glu	Gly	Ile	Trp	Asn	Asp	Met	Asn	
			405					410						415		
Glu	Pro	Ala	Val	Phe	Asn	Glu	Thr	Lys	Thr	Met	Asp	Val	Asn	Val	Val	
		420						425					430			
His	Arg	Gly	Asp	Gly	Arg	Leu	Tyr	Thr	His	Gly	Glu	Val	His	Asn	Leu	
		435				440					445					
Tyr	Gly	Phe	Trp	Met	Ala	Glu	Ala	Thr	Tyr	Arg	Gly	Leu	Lys	Ala	Gln	
	450				455						460					
Leu	Ala	Gly	Lys	Arg	Pro	Phe	Val	Leu	Thr	Arg	Ala	Gly	Tyr	Ser	Gly	
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Ile	Gln	Arg	Tyr	Ala	Ala	Val	Trp	Thr	Gly	Asp	Asn	Arg	Ser	Phe	Trp	
			485						490					495		
Glu	His	Met	Ala	Met	Ala	Ile	Pro	Met	Val	Leu	Asn	Met	Gly	Met	Ser	
		500						505					510			
Gly	Ile	Pro	Leu	Gly	Gly	Pro	Asp	Val	Gly	Gly	Phe	Ala	His	His	Ala	
	515					520						525				
Ser	Gly	Glu	Leu	Leu	Ala	Arg	Trp	Thr	Gln	Met	Gly	Ala	Phe	Phe	Pro	
	530					535					540					
Phe	Phe	Arg	Asn	His	Ser	Ala	Met	Gly	Thr	His	Arg	Gln	Glu	Pro	Trp	
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Ala	Phe	Gly	Pro	Thr	Phe	Glu	Ala	Val	Ile	Arg	Arg	Ala	Ile	Arg	Leu	
			565						570					575		
Arg	Tyr	Arg	Phe	Leu	Pro	Tyr	Leu	Tyr	Thr	Leu	Ala	Arg	Glu	Ala	His	
			580					585					590			
Glu	Thr	Gly	Leu	Pro	Met	Met	Arg	Pro	Leu	Val	Leu	Glu	Tyr	Pro	Asp	
	595						600					605				
Asp	Pro	Asn	Thr	His	His	Val	Asp	Asp	Gln	Phe	Leu	Val	Gly	Ser	Asp	
	610				615						620					
Leu	Leu	Val	Ala	Pro	Ile	Leu	Lys	Pro	Gly	Met	Ala	His	Arg	Met	Val	
	625				630					635					640	
Tyr	Leu	Pro	Asp	Gly	Glu	Trp	Ile	Asp	Tyr	Glu	Thr	Arg	Glu	Arg	Tyr	
			645						650					655		
Gln	Gly	Arg	Gln	Tyr	Ile	Leu	Thr	Tyr	Ala	Pro	Leu	Asp	Arg	Ile	Pro	
		660						665					670			
Leu	Tyr	Val	Arg	Ala	Gly	Ser	Ala	Ile	Pro	Val	Asn	Leu	Leu	Glu	Arg	
	675					680						685				
Ser	Gly	Glu	Thr	Gln	Leu	Gly	Trp	Glu	Ile	Phe	Val	Asp	Ala	Asn	Gly	
	690				695					700						
Arg	Ala	Ser	Gly	Arg	Cys	Tyr	Glu	Asp	Asp	Gly	Glu	Thr	Phe	Ser	Tyr	
705					710					715					720	
Glu	Asp	Gly	Ala	Tyr	Cys	Asp	Arg	Val	Leu	Gln	Ala	Leu	Ala	Thr	Ser	
			725						730					735		
Glu	Gly	Thr	Leu	Ile	Glu	Cys	His	Leu	Val	Gln	Gly	Ser	Gly	Asp	Gly	
		740						745					750			
Gly	Ser	Leu	Glu	Ser	Val	Val	Arg	Val	Phe	Thr	Pro	Asp	Asp	Val	Arg	
	755						760						765			

~~PC~~ ~~Glu~~ ~~Ala~~ ~~Arg~~ ~~Ala~~ ~~Gln~~ ~~Gly~~ ~~His~~ ~~Ser~~ ~~Phe~~ ~~Ser~~ ~~Leu~~ ~~His~~ ~~Val~~
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<210> 9

<211> 1611

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 9

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gatcttggcg	tggacgcggt	ctggctgtca	ccgttcttca	aaagcccgat	gaaggacatg	180
ggctatgacg	tcagcgacta	ttgcgatgtc	gatccgggtct	tcggcacccct	cgccgatttt	240
gacgccctgc	tggcccgcg	gcatgagctg	gggctcaagg	tgatcatcga	ccagggtcctt	300
agccacagtt	ccgacctgca	ccctgccttt	gtgaccagtc	gcagcgaccg	cgtgaacccg	360
aaggcggaact	ggtatgtctg	ggccgatccc	aagcccgacg	gcagcccgcc	caacaactgg	420
ctgtcgggtgt	tcgggtggctc	ggcatggggc	tgggacgcgc	gcagaaaaca	gtattacctg	480
cacaatttcc	tgaccagcca	gccggacctg	aactaccaca	acccgaaggt	gcaggactgg	540
gcgctggaca	acatgcgttt	ctggctggac	cggggcggtg	acgggttccg	ctttgacacc	600
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cctgaggctg	acggcaatcc	ctacggcatg	cagtaccacc	tgcattgaca	gaaccagccc	720
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gtcggcgaga	tgggcgaaag	tcaccacgcc	atccggatga	tgggcgacta	caccgctccg	840
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tgggagggcg	aggagctggg	ccagaccgat	accgaactgg	ccttggtatga	gttgaccgat	1140
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gtttggggacg	catcgccgca	tggcggtttt	tcgaccgtca	caccctggct	gccggtgaaa	1260
ccggaacagg	ccgcgcgtca	tgtggccggg	caaaccggtg	atgccgcctc	ggtgctggaa	1320
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cggtttcttg	atctggccga	accggttctg	ggctttgtgc	gcggcggaag	ggagggtgcg	1440
atcctgtgcc	tgttcaatct	gtcgctgttt	gcgcgggggg	ttgcggtcga	aggcggtgggc	1500
ccgccgatcg	gcccggggcca	gcaggctatc	ctttcgggcg	gacggctagg	ccttgggccc	1560
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<210> 10

<211> 536

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 10

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			20					25					30		
Thr	Ala	Arg	Leu	Glu	Tyr	Leu	Ala	Asp	Leu	Gly	Val	Asp	Ala	Val	Trp
		35					40					45			
Leu	Ser	Pro	Phe	Phe	Lys	Ser	Pro	Met	Lys	Asp	Met	Gly	Tyr	Asp	Val
	50					55					60				
Ser	Asp	Tyr	Cys	Asp	Val	Asp	Pro	Val	Phe	Gly	Thr	Leu	Ala	Asp	Phe
65					70				75					80	
Asp	Ala	Leu	Leu	Ala	Arg	Ala	His	Glu	Leu	Gly	Leu	Lys	Val	Ile	Ile
				85				90						95	
Asp	Gln	Val	Leu	Ser	His	Ser	Ser	Asp	Leu	His	Pro	Ala	Phe	Val	Thr
		100						105					110		
Ser	Arg	Ser	Asp	Arg	Val	Asn	Pro	Lys	Ala	Asp	Trp	Tyr	Val	Trp	Ala

Asp	Pro	Lys	Pro	Asp	Gly	Ser	Pro	Pro	Asn	Asn	Trp	Leu	Ser	Val	Phe
130						135					140				
Gly	Gly	Ser	Ala	Trp	Ala	Trp	Asp	Ala	Arg	Arg	Lys	Gln	Tyr	Tyr	Leu
145					150					155					160
His	Asn	Phe	Leu	Thr	Ser	Gln	Pro	Asp	Leu	Asn	Tyr	His	Asn	Pro	Lys
				165					170					175	
Val	Gln	Asp	Trp	Ala	Leu	Asp	Asn	Met	Arg	Phe	Trp	Leu	Asp	Arg	Gly
			180					185					190		
Val	Asp	Gly	Phe	Arg	Phe	Asp	Thr	Val	Asn	Tyr	Phe	Phe	His	Asp	Pro
		195					200					205			
Leu	Leu	Arg	Ser	Asn	Pro	Ala	Asp	His	Arg	Asn	Lys	Pro	Glu	Ala	Asp
		210					215				220				
Gly	Asn	Pro	Tyr	Gly	Met	Gln	Tyr	His	Leu	His	Asp	Lys	Asn	Gln	Pro
225					230					235					240
Glu	Asn	Leu	Ile	Trp	Met	Glu	Arg	Ile	Arg	Val	Leu	Leu	Asp	Gln	Tyr
				245					250					255	
Gly	Ala	Ala	Ser	Val	Gly	Glu	Met	Gly	Glu	Ser	His	His	Ala	Ile	Arg
			260					265					270		
Met	Met	Gly	Asp	Tyr	Thr	Ala	Pro	Gly	Arg	Leu	His	Gln	Cys	Tyr	Ser
		275					280					285			
Phe	Glu	Phe	Met	Gly	Tyr	Glu	Tyr	Thr	Ala	Asn	Leu	Phe	Arg	Asp	Arg
		290				295					300				
Ile	Glu	Ser	Phe	Phe	Lys	Gly	Ala	Pro	Lys	Gly	Trp	Pro	Met	Trp	Ala
305					310					315					320
Phe	Ser	Asn	His	Asp	Val	Val	Arg	His	Val	Ser	Arg	Trp	Ala	Lys	His
				325					330					335	
Gly	Leu	Thr	Pro	Glu	Ala	Val	Ala	Lys	Gln	Thr	Gly	Ala	Leu	Leu	Leu
			340					345					350		
Ser	Leu	Glu	Gly	Ser	Ile	Cys	Leu	Trp	Glu	Gly	Glu	Glu	Leu	Gly	Gln
		355					360					365			
Thr	Asp	Thr	Glu	Leu	Ala	Leu	Asp	Glu	Leu	Thr	Asp	Pro	Gln	Gly	Ile
		370					375				380				
Val	Phe	Trp	Pro	Glu	Pro	Ile	Gly	Arg	Asp	Asn	Thr	Arg	Thr	Pro	Met
385					390					395					400
Val	Trp	Asp	Ala	Ser	Pro	His	Gly	Gly	Phe	Ser	Thr	Val	Thr	Pro	Trp
				405					410					415	
Leu	Pro	Val	Lys	Pro	Glu	Gln	Ala	Ala	Arg	His	Val	Ala	Gly	Gln	Thr
			420					425				430			
Gly	Asp	Ala	Ala	Ser	Val	Leu	Glu	Ser	Tyr	Arg	Ala	Met	Leu	Ala	Phe
		435					440				445				
Arg	Arg	Ala	Glu	Pro	Ala	Leu	Arg	Thr	Gly	Arg	Thr	Arg	Phe	Leu	Asp
		450				455					460				
Leu	Ala	Glu	Pro	Val	Leu	Gly	Phe	Val	Arg	Gly	Glu	Gly	Glu	Gly	Ala
465					470					475					480
Ile	Leu	Cys	Leu	Phe	Asn	Leu	Ser	Pro	Val	Ala	Arg	Gly	Val	Ala	Val
				485					490					495	
Glu	Gly	Val	Gly	Pro	Pro	Ile	Gly	Pro	Gly	Gln	Gln	Ala	Ile	Leu	Ser
			500					505					510		
Gly	Gly	Arg	Leu	Gly	Leu	Gly	Pro	Asn	Gly	Ala	Ala	Phe	Leu	Arg	Val
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Thr	Gly	Thr	Val	Arg	Val	Leu	Asp								
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<210> 11

<211> 1719

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 11

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gattgcggct acgatatcag cgattaccgc aacgttgctc cggaatacgg cagcgtggac 240
gatttcaaaa ccttcctgag cgaatcgac aaacgcggta tccgcgtcat tctcgacctc 300
gtgctgaatc acacctccga tgaacatccg tgggtcatcg aatcgaaatc cagccgcgat 360
aatcccaaat ccgattggta tgtgtgggtc gatacgccgc ccaacaattg gcagtcctgc 420
ttcgatggcg atgcctggac atacgtccct gaacgcggcc aatattatta tcactacttc 480
atgaaacagc agcccgatct caactggcat aatccgcagg tcaaacaggc catgtgggag 540
gcggtgcgct tctggctcga tctcggcgtg gacggcttcc gcctggacgc catcggcacg 600
atctacgaag acccaaatct cagcccgcat aatgtcccga tgaatttggc tgagctgcgt 660
cacttcacag atgtcgccaa aacgcccggaa gagatcaagc tcaaagaaaa atactggcac 720
gacatgttca agcatcaatg gggtcagccc ggcgttcatg acctgatgaa agaactgcgc 780
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cacatcatta ccgatcccac caaactgcgc gacaccatgg caacctggta ttacaacagc 1200
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gataaagccg aacctgggtt gccagtcaac cccaattacc gcgcaggcat taacgtccgc 1380
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<210> 12

<211> 572

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 12

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20          25          30
Gly Ile Ile Gly Lys Leu Asp Tyr Leu Gln Asn Leu Gly Ile Asp Ala
35          40          45
Leu Trp Leu Ser Pro His Phe Pro Ser Pro Asn Trp Asp Cys Gly Tyr
50          55          60
Asp Ile Ser Asp Tyr Arg Asn Val Ala Pro Glu Tyr Gly Thr Leu Asp
65          70          75          80
Asp Phe Lys Thr Phe Leu Ser Glu Ser His Lys Arg Gly Ile Arg Val
85          90          95
Ile Leu Asp Leu Val Leu Asn His Thr Ser Asp Glu His Pro Trp Phe
100          105          110
Ile Glu Ser Lys Ser Ser Arg Asp Asn Pro Lys Ser Asp Trp Tyr Val
115          120          125
Trp Val Asp Thr Pro Pro Asn Asn Trp Gln Ser Cys Phe Asp Gly Asp
130          135          140
Ala Trp Thr Tyr Val Pro Glu Arg Gly Gln Tyr Tyr Tyr His Tyr Phe
145          150          155          160
Met Lys Gln Gln Pro Asp Leu Asn Trp His Asn Pro Gln Val Lys Gln
165          170          175
Ala Met Trp Glu Ala Val Arg Phe Trp Leu Asp Leu Gly Val Asp Gly
180          185          190
Phe Arg Leu Asp Ala Ile Gly Thr Ile Tyr Glu Asp Pro Asn Leu Thr
195          200          205

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PC Pro His Asp Val Pro Met Asn Ile Ala Glu Leu Arg His Phe Thr Asp
 210 215 220
 Val Ala Lys Thr Pro Glu Ile Lys Leu Lys Glu Lys Tyr Trp His
 225 230 235
 Asp Met Phe Lys His Gln Trp Gly Gln Pro Gly Val His Asp Leu Met
 245 250 255
 Lys Glu Leu Arg Ala Ile Leu Asp Glu Tyr Asp Gly Asp Arg Met Leu
 260 265 270
 Val Gly Glu Asp Asp Asn Ile Asp Tyr Met Gly Asn Gly Asp Asp Glu
 275 280 285
 Leu Gln Leu Val Phe Asn Phe Pro Leu Met Arg Ala Asp Arg Leu Thr
 290 295 300
 Pro Asp His Ile Arg Arg Asn Gln Lys Glu Arg Leu Thr Arg Leu Asn
 305 310 315
 Ala Leu Pro Val Lys Gly Trp Ala Cys Asn Thr Leu Gly Asn His Asp
 325 330 335
 Ser Ser Arg Val Tyr Thr Lys Phe Gly Asp Arg Ile His Gly Ala Asp
 340 345 350
 His Ala Arg Leu Asn Leu Ala Leu Leu Leu Thr Leu His Gly Thr Pro
 355 360 365
 Phe Leu Tyr Asn Gly Glu Glu Ile Gly Met Thr Asp His Ile Ile Thr
 370 375 380
 Asp Pro Thr Lys Leu Arg Asp Thr Met Ala Thr Trp Tyr Tyr Asn Ser
 385 390 395
 Leu Val Asn Glu Met Lys Val Glu Pro Ala Glu Ala Ala Leu Arg Ala
 405 410 415
 Gly Gln Met Thr Arg Asp Lys Asn Arg Thr Pro Met Gln Trp Asp Asn
 420 425 430
 Lys Pro Asn Ala Gly Phe Cys Pro Asp Lys Ala Glu Pro Trp Leu Pro
 435 440 445
 Val Asn Pro Asn Tyr Arg Ala Gly Ile Asn Val Arg Glu Gln Thr Ser
 450 455 460
 Asn Pro Asn Ser Leu Leu Asn Tyr Tyr Lys Arg Leu Ile His Leu Arg
 465 470 475
 Arg Glu Thr Pro Ala Leu Ile Ala Gly Asp Tyr Val Pro Leu His Gln
 485 490 495
 Thr Ser Lys Asp His Leu Ala Phe Leu Arg Lys Thr Asp Ser Gln Thr
 500 505 510
 Ile Leu Val Val Leu Asn Tyr Ser Pro Asn Lys Leu Glu Leu Asp Phe
 515 520 525
 Ser Arg Thr Val Glu Met Lys Gly Arg Pro Leu Ile Ala Ile Phe Ser
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 Ser Ala Asp Asp Arg Pro Gln Ala Ala Gln Ser Pro Lys Lys Val Ser
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<210> 13
 <211> 1392
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

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 atttacctca tggatatcaa taaggagcgc ctgcacctca taacagggtt cgccaagcga 180
 tacgctgccg agatgcacgc tgatctagag ttcattccga caatggatcg tgtcgaagcg 240
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 cggatgaggg aaatatgtga gagacacggc tattacaggg gaataaata tagtctgagtgg 360
 aacatggtca gcgactacca caccatatgg ggctactacc agttcaaact agcactaagc 420
 attgccaagg acgtcgagga ttacgctccc gatgcatggc ttatcaacgt cgctaatacca 480

~~gtgttccgaat~~ ~~tgacaacact~~ ~~gatccagagg~~ ~~taacggaaga~~ taaagatgat agggctgtgc 540
catggatacc acggcatata taatgtcatg aaagaactag gcctaccacg agaagaaaca 600
gagttcgagg tactaggatt caaccacgtc atatggctta caaagttcaa gtaccaggga 660
gaagacgctt acccgttact agacaagtgg atcgaggaga aagcagagaa gtactgggag 720
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tccatagtcc caataatcga tagcctcgcc aacaatagga ggggagaata cgttatcaac 1080
acgttgaatc tgggcagcat acccgggata cgggataatg tggctgtcga gatgccggcc 1140
cagatagatg gtaaaggagt gcaccgctac atattcgagc cactcccaa gaagataaga 1200
gacctggctc tactgcctag gatgaccgt atggagatgg cattgacagc cttcctcgag 1260
ggaggccgtg aagtactaga ggactggcta cacatggatc cacgtaccaa gagcactaga 1320
caggtaacggg agacaatcga tgatctcctt aacatgcccc gtaacgagga gatgaagaag 1380
catttcagct aa 1392

<210> 14
<211> 463
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 14
Met Glu Glu Glu Pro Arg Gly Lys Gly Leu Lys Ile Ala Phe Ile Gly
1 5 10 15
Ala Gly Ser Ala Val Trp Ser Ser Arg Ile Ile Val Asp Leu Ile Leu
20 25 30
Ala Lys Ser Leu His Gly Ala Lys Ile Tyr Leu Met Asp Ile Asn Lys
35 40 45
Glu Arg Leu Asp Leu Ile Thr Gly Phe Ala Lys Arg Tyr Ala Ala Glu
50 55 60
Met His Ala Asp Leu Glu Phe Ile Pro Thr Met Asp Arg Val Glu Ala
65 70 75 80
Ile Arg Asp Ala Asp Phe Val Val Asn Ser Ala Met Tyr Gly Gly His
85 90 95
Met Tyr Tyr Glu Arg Met Arg Glu Ile Cys Glu Arg His Gly Tyr Tyr
100 105 110
Arg Gly Ile Asn Ser Val Glu Trp Asn Met Val Ser Asp Tyr His Thr
115 120 125
Ile Trp Gly Tyr Tyr Gln Phe Lys Leu Ala Leu Ser Ile Ala Lys Asp
130 135 140
Val Glu Asp Tyr Ala Pro Asp Ala Trp Leu Ile Asn Val Ala Asn Pro
145 150 155 160
Val Phe Glu Leu Thr Thr Leu Ile Gln Arg His Val Lys Ile Lys Met
165 170 175
Ile Gly Leu Cys His Gly Tyr His Gly Ile Tyr Asn Val Met Lys Glu
180 185 190
Leu Gly Leu Pro Arg Glu Glu Thr Glu Phe Glu Val Leu Gly Phe Asn
195 200 205
His Val Ile Trp Leu Thr Lys Phe Lys Tyr Gln Gly Glu Asp Ala Tyr
210 215 220
Pro Leu Leu Asp Lys Trp Ile Glu Glu Lys Ala Glu Lys Tyr Trp Glu
225 230 235 240
His Trp Arg Gln Thr Gln Val Asn Pro Phe Asp Ile Asp Leu Ser Pro
245 250 255
Ala Ala Ile Asp Met Tyr Lys Arg Tyr Gly Leu Leu Pro Val Gly Asp
260 265 270
Thr Val Arg Gly Gly Thr Trp Met Tyr His Trp Asp Leu Lys Thr Lys
275 280 285
Gln Lys Trp Tyr Gly Pro Thr Gly Gly Pro Asp Ser Glu Ile Gly Trp
290 295 300

PC Met Met Tyr Ile Ala Phe Leu Ser Met Gln Leu Gln Arg Leu Tyr Glu
 305 310 315 320
 Ala Leu Thr Asp Gln Lys His Pro Leu Ala Ala His Val Pro Pro Glu
 325 330 335
 Trp Ser Gly Glu Ser Ile Val Pro Ile Ile Asp Ser Leu Ala Asn Asn
 340 345 350
 Arg Arg Gly Glu Tyr Val Ile Asn Thr Leu Asn Leu Gly Ser Ile Pro
 355 360 365
 Gly Ile Pro Asp Asn Val Ala Val Glu Met Pro Ala Gln Ile Asp Gly
 370 375 380
 Lys Gly Val His Arg Tyr Ile Phe Glu Pro Leu Pro Lys Lys Ile Arg
 385 390 395 400
 Asp Leu Val Leu Leu Pro Arg Met Thr Arg Met Glu Met Ala Leu Thr
 405 410 415
 Ala Phe Leu Glu Gly Gly Arg Glu Val Leu Glu Asp Trp Leu His Met
 420 425 430
 Asp Pro Arg Thr Lys Ser Thr Arg Gln Val Arg Glu Thr Ile Asp Asp
 435 440 445
 Leu Leu Asn Met Pro Gly Asn Glu Glu Met Lys Lys His Phe Ser
 450 455 460

<210> 15
 <211> 1632
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 15
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 gcgtcgatct accagattta cccgcgcagt tttgcggaca gcaacgggtga tggcggtggc 120
 gaccttgccg ggattacttc gcatctggag catatcgca gcctgggtgt ggaggcgatc 180
 tggatcagcc cgtttttcac cagcccgatg gccgattatg gctatgacgt ggcggattat 240
 tgcatgtcg atccgatctt cgggactttg gcggacttcg atgcgctggg cgagaaggcc 300
 catgggctgg gcctgaaggt caccatcgac atggtctttg cccataccag cgacaggcat 360
 ccgtgggtcg aacaatcgcg ttcggcgcgc gagaatgacc gcgccgactg gtacgtctgg 420
 gccgatccca agccggacgg cagccgcgcc aacaactggc agtcgggtgt tggcggcccg 480
 gcctggacct gggacgcgcg gcgcgggcag tactacatgc accagttcct gaaggagcag 540
 ccgcaattga acgcgcacaa tcctgcggtg caggatgcgc tgctcgatgc cttgcgcttc 600
 tggctggagc ggggggtgga cgggttcggg ctcgatgcgc tgaaccactc gatgttcgat 660
 ccggcgctga ccgacaatct gcccgcgccc gaggatggca agatccgcac gcggcctttc 720
 gattttcagt tgaaaatcaa cagccagaac catcccgtg tgacgctgtt catcgagcgg 780
 atcgccgatg tttgcggcca gcatggcgcg gtcttcaccg tggccgaagt gggcgcgat 840
 ggcgcgggtc cgctgatgaa ggcgtacacg gcgggcgagc atcggtgtc ctcggcctac 900
 agctttgatt tcctttatgc gccggccttg acgggcgagc tgggtggcaa tgctctggcc 960
 cagtggacgg gcaagccggg ggccgatggg ctgagcgaag gctggcccag ctgggcgttt 1020
 gagaaccatg atgcgcccg ccatatctcg cgctgggtgg gcgaggagca tcgcgccgcc 1080
 tttgcccgga tgagccttgt gctgctggcc tcgctgcgcg gtaacatgtt catgtatcag 1140
 gggcaggaac tggcgctgga gcaggatgag atcccgtttc atctgctgaa agaccccgag 1200
 gcgatcgcca actggccgct gacgttgagc cgcgacgggg tgcgcacgcc gatgccatgg 1260
 gacagccagg ccttccatgc cggcttcacg agtggcgagc cctggttgcc cttgtcgccg 1320
 ggggaatatcg ccaaggcggt ggatgtgcag gaggccgatc cgcagagcca gctgcactgg 1380

 gtgcggcggg ttctggccct gcgcgcgcgg cacaaggccc tgcgtctggg cgcgatggag 1440
 catgtgcatt tgcagggcga tgtgctcagt ttcaccgcgc atgcgcgcgg cgaaagggtg 1500
 gagtgcgtgt tcaacctttc cgccaaaacc gtcgccaca aggcgcacaa gggtagacg 1560
 ctgctcaccg tcaatggcgc aaccggggcg gtgttgacgc catatggcgc tctctggacg 1620
 aaactcgcat aa 1632

<210> 16
 <211> 543
 <212> PRT

<220>

<223> Obtained from an environmental sample

<400> 16

Met	Thr	Gln	Ser	Ser	Ser	Ala	Val	Ser	Pro	Ala	Ser	Ser	Gly	Pro	Ala
1				5					10					15	
Trp	Trp	His	Gly	Ala	Ser	Ile	Tyr	Gln	Ile	Tyr	Pro	Arg	Ser	Phe	Ala
		20						25					30		
Asp	Ser	Asn	Gly	Asp	Gly	Val	Gly	Asp	Leu	Ala	Gly	Ile	Thr	Ser	His
		35					40					45			
Leu	Glu	His	Ile	Ala	Ser	Leu	Gly	Val	Glu	Ala	Ile	Trp	Ile	Ser	Pro
	50					55					60				
Phe	Phe	Thr	Ser	Pro	Met	Ala	Asp	Tyr	Gly	Tyr	Asp	Val	Ala	Asp	Tyr
65				70					75						80
Cys	Asp	Val	Asp	Pro	Ile	Phe	Gly	Thr	Leu	Ala	Asp	Phe	Asp	Ala	Leu
				85					90					95	
Val	Glu	Lys	Ala	His	Gly	Leu	Gly	Leu	Lys	Val	Thr	Ile	Asp	Met	Val
			100					105					110		
Phe	Ala	His	Thr	Ser	Asp	Arg	His	Pro	Trp	Phe	Glu	Gln	Ser	Arg	Ser
		115				120						125			
Ala	Arg	Glu	Asn	Asp	Arg	Ala	Asp	Trp	Tyr	Val	Trp	Ala	Asp	Pro	Lys
	130					135					140				
Pro	Asp	Gly	Thr	Pro	Pro	Asn	Asn	Trp	Gln	Ser	Val	Phe	Gly	Gly	Pro
145				150					155						160
Ala	Trp	Thr	Trp	Asp	Ala	Arg	Arg	Gly	Gln	Tyr	Tyr	Met	His	Gln	Phe
				165				170						175	
Leu	Lys	Glu	Gln	Pro	Gln	Leu	Asn	Ala	His	Asn	Pro	Ala	Val	Gln	Asp
			180					185					190		
Ala	Leu	Leu	Asp	Ala	Leu	Arg	Phe	Trp	Leu	Glu	Arg	Gly	Val	Asp	Gly
		195					200					205			
Phe	Arg	Leu	Asp	Ala	Leu	Asn	His	Ser	Met	Phe	Asp	Pro	Ala	Leu	Thr
	210					215					220				
Asp	Asn	Leu	Pro	Ala	Pro	Glu	Asp	Gly	Lys	Ile	Arg	Thr	Arg	Pro	Phe
225				230					235						240
Asp	Phe	Gln	Leu	Lys	Ile	Asn	Ser	Gln	Asn	His	Pro	Ala	Val	Thr	Leu
				245					250					255	
Phe	Ile	Glu	Arg	Ile	Ala	Asp	Val	Cys	Gly	Gln	His	Gly	Ala	Val	Phe
			260					265					270		
Thr	Val	Ala	Glu	Val	Gly	Gly	Asp	Gly	Ala	Val	Pro	Leu	Met	Lys	Ala
		275					280					285			
Tyr	Thr	Ala	Gly	Glu	His	Arg	Leu	Ser	Ser	Ala	Tyr	Ser	Phe	Asp	Phe
	290					295					300				
Leu	Tyr	Ala	Pro	Ala	Leu	Thr	Gly	Glu	Leu	Val	Ala	Asn	Ala	Leu	Ala
305					310				315						320
Gln	Trp	Thr	Gly	Lys	Pro	Gly	Ala	Asp	Gly	Leu	Ser	Glu	Gly	Trp	Pro
				325					330					335	
Ser	Trp	Ala	Phe	Glu	Asn	His	Asp	Ala	Pro	Arg	His	Ile	Ser	Arg	Trp
			340					345					350		
Val	Gly	Glu	Glu	His	Arg	Ala	Ala	Phe	Ala	Arg	Met	Ser	Leu	Val	Leu
		355				360						365			
Leu	Ala	Ser	Leu	Arg	Gly	Asn	Met	Phe	Met	Tyr	Gln	Gly	Gln	Glu	Leu
	370					375					380				
Ala	Leu	Glu	Gln	Asp	Glu	Ile	Pro	Phe	His	Leu	Leu	Lys	Asp	Pro	Glu
385					390					395					400
Ala	Ile	Ala	Asn	Trp	Pro	Leu	Thr	Leu	Ser	Arg	Asp	Gly	Val	Arg	Thr
				405					410					415	
Pro	Met	Pro	Trp	Asp	Ser	Gln	Ala	Phe	His	Ala	Gly	Phe	Thr	Ser	Gly
			420					425					430		
Glu	Pro	Trp	Leu	Pro	Leu	Ser	Pro	Gly	Asn	Ile	Ala	Lys	Ala	Val	Asp
		435					440					445			
Val	Gln	Glu	Ala	Asp	Pro	Gln	Ser	Gln	Leu	His	Trp	Val	Arg	Arg	Val
	450					455					460				

P C Leu Ala Glu Arg Val Ala Arg His Lys Ala Leu Arg Leu Gly Ala Met Glu
 465 470 475 480
 His Val His Val Gln Gly Asp Val Leu Ser Phe Thr Arg His Ala Arg
 485 490 495
 Gly Glu Arg Val Glu Cys Val Phe Asn Leu Ser Ala Lys Thr Val Ala
 500 505 510
 His Lys Ala His Lys Gly Glu Thr Leu Leu Thr Val Asn Gly Ala Thr
 515 520 525
 Gly Ala Val Leu Thr Pro Tyr Gly Ala Leu Trp Thr Lys Leu Ala
 530 535 540

<210> 17
 <211> 1392
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 17
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 gtctatctca tggatattaa taaggagcgg ctcgacctca taacagggtt cgccaagcga 180
 tacgctgccg agatgcatgc tgatctagag tttatcccta caatggatcg catagaggcg 240
 ataagggatg cagacttcgt cgtcaactca gccatgtacg gtggccacat gtactatgag 300
 cgtatgagag aaatatgtga gaggcacggc tattaccgag gaataaacag tgttgaatgg 360
 aacatggtca gcgattacca caccatatgg ggttactacc agttcaaact agccatgagc 420
 attgccaaag atgtagagga atacgcgccc gacgcctggc ttatcaacgt cgccaaccct 480
 gtgttcgagc tgacaacact gatccagagg cacgtcaaga taaagatgat agggctctgc 540
 catggctacc atggcatcta taatgtgatc aaagaactcg ggctagacag ggatgagaca 600
 gagttcgagg tactcggtt caaccatgtg atctggctca caaagttcaa gtacagggga 660
 gaggacgctt accccttact agataagtgg atcgaggaga aagcagagaa gtactgggag 720
 cattggagac aaacacaggt gaaccgcgtt gacattgact tgtctcctgc agcgatagac 780
 atgtacaaga gatacgggtc acttccggta ggagatactg tgcgtggagg cacgtggatg 840
 taccactggg atctcaagac gaagcagaaa tggatatggac cgacaggagg accagactcc 900
 gagataggct ggatgatgta tatagccttc ctaagcatgc agtcctcaaag attatacgaa 960
 gcactaatgg atcagaagca cccattagca gcacatatat cgccggagtg gagcgggtgaa 1020
 tccatagttc caataatcga tagcctcgcc aacaatagga ggggagaata cgttatcaac 1080
 acgttgaacc ttggtagtat accggggata ccggatagtg tagctgtcga gatgccagcc 1140
 cagatagatg gtaaaggagt gcaccgctac atattcgagc ccctcccca gaagataaga 1200
 gacctagtcc tactgcctag gatgaccgt atggagatgg cgttgacagc cttcctcgag 1260
 ggaggccgag aagtactcga ggactggcta cacatggatc cacgtaccaa gagcactgga 1320
 caggtacggg agacaatcga tgatctcctg aacatgcccg gtaacgagga gatgaagaag 1380
 catttcagct ag 1392

<210> 18
 <211> 463
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 18
 Met Glu Glu Glu Pro Arg Gly Lys Gly Leu Lys Ile Ala Phe Ile Gly
 1 5 10 15
 Ala Gly Ser Ala Val Trp Ser Ser Arg Ile Ile Ile Asp Leu Ile Leu
 20 25 30
 Ala Lys Ser Leu His Gly Ala Lys Val Tyr Leu Met Asp Ile Asn Lys
 35 40 45
 Glu Arg Leu Asp Leu Ile Thr Gly Phe Ala Lys Arg Tyr Ala Ala Glu
 50 55 60
 Met His Ala Asp Leu Glu Phe Ile Pro Thr Met Asp Arg Ile Glu Ala
 65 70 75 80

PC Ile Arg Asp Ala Asn Phe Val Val Asn Ser Ala Met Tyr Gly Gly His
 85 90 95
 Met Tyr Tyr Glu Arg Met Arg Glu Ile Cys Glu Arg His Gly Tyr Tyr
 100 105 110
 Arg Gly Ile Asn Ser Val Glu Trp Asn Met Val Ser Asp Tyr His Thr
 115 120 125
 Ile Trp Gly Tyr Tyr Gln Phe Lys Leu Ala Met Ser Ile Ala Lys Asp
 130 135 140
 Val Glu Glu Tyr Ala Pro Asp Ala Trp Leu Ile Asn Val Ala Asn Pro
 145 150 155 160
 Val Phe Glu Leu Thr Thr Leu Ile Gln Arg His Val Lys Ile Lys Met
 165 170 175
 Ile Gly Leu Cys His Gly Tyr His Gly Ile Tyr Asn Val Ile Lys Glu
 180 185 190
 Leu Gly Leu Asp Arg Asp Glu Thr Glu Phe Glu Val Leu Gly Phe Asn
 195 200 205
 His Val Ile Trp Leu Thr Lys Phe Lys Tyr Arg Gly Glu Asp Ala Tyr
 210 215 220
 Pro Leu Leu Asp Lys Trp Ile Glu Glu Lys Ala Glu Lys Tyr Trp Glu
 225 230 235 240
 His Trp Arg Gln Thr Gln Val Asn Pro Phe Asp Ile Asp Leu Ser Pro
 245 250 255
 Ala Ala Ile Asp Met Tyr Lys Arg Tyr Gly Leu Leu Pro Val Gly Asp
 260 265 270
 Thr Val Arg Gly Gly Thr Trp Met Tyr His Trp Asp Leu Lys Thr Lys
 275 280 285
 Gln Lys Trp Tyr Gly Pro Thr Gly Gly Pro Asp Ser Glu Ile Gly Trp
 290 295 300
 Met Met Tyr Ile Ala Phe Leu Ser Met Gln Leu Gln Arg Leu Tyr Glu
 305 310 315 320
 Ala Leu Met Asp Gln Lys His Pro Leu Ala Ala His Ile Pro Pro Glu
 325 330 335
 Trp Ser Gly Glu Ser Ile Val Pro Ile Ile Asp Ser Leu Ala Asn Asn
 340 345 350
 Arg Arg Gly Glu Tyr Val Ile Asn Thr Leu Asn Leu Gly Ser Ile Pro
 355 360 365
 Gly Ile Pro Asp Ser Val Ala Val Glu Met Pro Ala Gln Ile Asp Gly
 370 375 380
 Lys Gly Val His Arg Tyr Ile Phe Glu Pro Leu Pro Lys Lys Ile Arg
 385 390 395 400
 Asp Leu Val Leu Leu Pro Arg Met Thr Arg Met Glu Met Ala Leu Thr
 405 410 415
 Ala Phe Leu Glu Gly Gly Arg Glu Val Leu Glu Asp Trp Leu His Met
 420 425 430
 Asp Pro Arg Thr Lys Ser Thr Gly Gln Val Arg Glu Thr Ile Asp Asp
 435 440 445
 Leu Leu Asn Met Pro Gly Asn Glu Glu Met Lys Lys His Phe Ser
 450 455 460

<210> 19

<211> 1686

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 19

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aaaaagctcg	gggtagatgt	tctgtggcta	acgccaattt	ataaatcacc	gcagcgggat	180
aatggatatg	atataagtga	ttattttgtt	attcaagaag	aatacggaac	aatggaggat	240
tttgatcttt	tagtaacaga	agcgcataag	cggggtctta	aagtcatcat	ggatattgtc	300
gttaatcata	catcaactga	acatgaatgg	tttcaagaag	ctaaaaaatc	gaaagataac	360

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PC "tcgtacccgag"attttttatatctgggaaggtc"caaaaaggaa" atggaagtgc tccgacgaat 420
tgggttttcaa aatttggggg atccgcgtgg gagcatgata acctcacaga acaatcgtat 480
ctgcatttgt ttgatgttac gcaagcggat ttgaactggg aaaacgagcg tgtgcgccgc 540
agcgtgtatg atatgatgac gtttttggtt gaaaaaggag tagatggatt tcgtctggac 600
gttattaatt taatttcaaa agatcagcgt ttttttagatg atgacgggtc cgttgcacca 660
ggagatggcc ggaaattcta caccgacggt cctcgcgtgc acgaatatat gcgggaaatg 720
aatcaagaag ttttttcaaa atatgatagt atgaccgttg gagaaatgtc gtccacaacc 780
gttgaccact gtattcagta ctctcatccg gaccgacgcg agcttagtat gacgtttaat 840
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tttattaaat taaaagagat tctatcaact tggcaaacgg aaatgaataa aggtggggga 960
tggaatgcat tattttggtg caaccatgat cagcctcgcg ttgtttcacg ctatggagac 1020
gacgaactct atcataataa atctgctaaa atgctcgcga caacgattca tttgatgcag 1080
ggaacgcctt atatctatca aggcgaagaa ataggtatga caaacccgaa gttttcctct 1140
attgatgaat atagagatgt ggagtcattt aatgtgtatg aaataaaacg tgcacaagga 1200
atggacgaaa atgaaatttt ggaaatttta aaacataaat caagagataa ttcccgtaca 1260
ccggtgcaat ggaacgataa gccgaatgca ggttttaca aaggaaagcc atggattcat 1320
ccggccgata actaccgtaa aattaatgta gaaaaagcgt tagaggataa agattcaatc 1380
ttttattttt atcaaaagct tattgcactg cgcaagcagt acgagattat cacctatgga 1440
aactatgaat tgattcttgg agaagacgag cagattttcg cttatatccg aaatggagca 1500
gatgaaaagc tgctcgtgat aaacaatttc tacggcagcg agaaaatttt tgaactgcca 1560
gaaaatctaa cttttgaagg atatcatagt gaaatattgc tgtctaacta cgaagattca 1620
ccaaaggaat tcaagcgagt cttacttcgg ccgtatgaat caatcgtgta tcatttataaa 1680
aaatag 1686

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<210> 20
 <211> 561
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

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<400> 20
Met Gln Glu Pro Trp Trp Lys Lys Ser Val Val Tyr Gln Ile Tyr Pro
1          5          10          15
Lys Ser Phe Tyr Asp Thr Thr Gly Asn Gly Val Gly Asp Ile Ala Gly
20          25          30
Ile Ile Glu Lys Leu Asp Tyr Leu Lys Lys Leu Gly Val Asp Val Leu
35          40          45
Trp Leu Thr Pro Ile Tyr Lys Ser Pro Gln Arg Asp Asn Gly Tyr Asp
50          55          60
Ile Ser Asp Tyr Phe Val Ile Gln Glu Glu Tyr Gly Thr Met Glu Asp
65          70          75          80
Phe Asp Leu Leu Val Thr Glu Ala His Lys Arg Gly Leu Lys Val Ile
85          90          95

Met Asp Ile Val Val Asn His Thr Ser Thr Glu His Glu Trp Phe Gln
100          105          110
Glu Ala Lys Lys Ser Lys Asp Asn Pro Tyr Arg Asp Phe Tyr Ile Trp
115          120          125
Lys Asp Gln Lys Glu Asp Gly Ser Ala Pro Thr Asn Trp Val Ser Lys
130          135          140
Phe Gly Gly Ser Ala Trp Glu His Asp Asn Leu Thr Glu Gln Ser Tyr
145          150          155          160
Leu His Leu Phe Asp Val Thr Gln Ala Asp Leu Asn Trp Glu Asn Glu
165          170          175
Arg Val Arg Arg Ser Val Tyr Asp Met Met Thr Phe Trp Phe Glu Lys
180          185          190
Gly Val Asp Gly Phe Arg Leu Asp Val Ile Asn Leu Ile Ser Lys Asp
195          200          205
Gln Arg Phe Leu Asp Asp Asp Gly Ser Val Ala Pro Gly Asp Gly Arg
210          215          220
Lys Phe Tyr Thr Asp Gly Pro Arg Val His Glu Tyr Met Arg Glu Met
225          230          235          240

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P C Asn Glu Glu Val Phe Ser Lys Tyr Asp Ser Met Thr Val Gly Glu Met
 245 250 255
 Ser Ser Thr Thr Val Asp His Cys Ile Gln Tyr Ser His Pro Asp Arg
 260 265 270
 Arg Glu Leu Ser Met Thr Phe Asn Phe His His Leu Lys Val Asp Tyr
 275 280 285
 Pro Asn Gly Glu Lys Trp Ala Leu Ala Asp Phe Asp Phe Ile Lys Leu
 290 295 300
 Lys Glu Ile Leu Ser Thr Trp Gln Thr Glu Met Asn Lys Gly Gly Gly
 305 310 315 320
 Trp Asn Ala Leu Phe Trp Cys Asn His Asp Gln Pro Arg Val Val Ser
 325 330 335
 Arg Tyr Gly Asp Asp Glu Leu Tyr His Asn Lys Ser Ala Lys Met Leu
 340 345 350
 Ala Thr Thr Ile His Leu Met Gln Gly Thr Pro Tyr Ile Tyr Gln Gly
 355 360 365
 Glu Glu Ile Gly Met Thr Asn Pro Lys Phe Ser Ser Ile Asp Glu Tyr
 370 375 380
 Arg Asp Val Glu Ser Leu Asn Val Tyr Glu Ile Lys Arg Ala Gln Gly
 385 390 395 400
 Met Asp Glu Asn Glu Ile Leu Glu Ile Leu Lys His Lys Ser Arg Asp
 405 410 415
 Asn Ser Arg Thr Pro Val Gln Trp Asn Asp Lys Pro Asn Ala Gly Phe
 420 425 430
 Thr Lys Gly Lys Pro Trp Ile His Pro Ala Asp Asn Tyr Arg Lys Ile
 435 440 445
 Asn Val Glu Lys Ala Leu Glu Asp Lys Asp Ser Ile Phe Tyr Phe Tyr
 450 455 460
 Gln Lys Leu Ile Ala Leu Arg Lys Gln Tyr Glu Ile Ile Thr Tyr Gly
 465 470 475 480
 Asn Tyr Glu Leu Ile Leu Gly Glu Asp Glu Gln Ile Phe Ala Tyr Ile
 485 490 495
 Arg Asn Gly Ala Asp Glu Lys Leu Leu Val Ile Asn Asn Phe Tyr Gly
 500 505 510
 Ser Glu Lys Ile Phe Glu Leu Pro Glu Asn Leu Thr Phe Glu Gly Tyr
 515 520 525
 His Ser Glu Ile Leu Leu Ser Asn Tyr Glu Asp Ser Pro Lys Glu Phe
 530 535 540
 Lys Arg Val Leu Leu Arg Pro Tyr Glu Ser Ile Val Tyr His Leu Lys
 545 550 555 560
 Lys

<210> 21
 <211> 1443
 <212> DNA
 <213> Eukaryote

<400> 21
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 gtgagcgacc ttgcaaaac tcccgggtctt tccggaagta ccgttaccct catggacatc 120
 gacgaagaaa ggctagatgc ggttctgacc atagcaaaaa agtacgttga agaagtggga 180
 gccgacctga agtttgaaaa gacaacaagc gtagacgaag ccatcgctga tgcggatttt 240
 gtgataaaca cagcgatggg ggggtggccac acctatcttg aaaaggtcag aaggatcagc 300
 gaaaagtacg gatactacag aggaatagac ggcgaggagt tcaacatggg ctccgactac 360
 tacacgtttt caaactacaa ccagctcaag tacttcgtgg atatcgcaag gaaaatagag 420
 agactctctc caaaggcgtg gtatctgcag gcggc aaatc ctgtctttga aggaacaacc 480
 cttgtgacaa gaacggttcc cataaaggca gtgggattct gccatggaca ctacggcgtg 540
 atggagatcg tagagaaact ggggctggaa gaaaacaggg tagactggca ggttgccggt 600
 gtgaaccacg gaatatgggt gaacagggtc agatacaacg gcgaggatgc gtaccactt 660
 ctagatagat ggatcagtga aaaatcgaaa gactggaaac cagagaaccc cttcaacgac 720
 cagctctctc ccgctgcgat agacatgtac agattctacg gtgtgatgcc catcggtgac 780
 accgtgagaa actcttcgtg gaggtaccac agggatcttg agaccaagaa gaaatggtac 840
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P C GGAAGGTA CCGAGATCAC AAGGAGGTG GGAAGGTA tcaaagaaaa tccgtccgcg 960
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<210> 22
 <211> 480
 <212> PRT
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<400> 22

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Ser Thr Val Thr Leu Met Asp Ile Asp Glu Glu Arg Leu Asp Ala Val
 35          40          45
Leu Thr Ile Ala Lys Lys Tyr Val Glu Glu Val Gly Ala Asp Leu Lys
 50          55          60
Phe Glu Lys Thr Thr Ser Val Asp Glu Ala Ile Ala Asp Ala Asp Phe
 65          70          75          80
Val Ile Asn Thr Ala Met Val Gly Gly His Thr Tyr Leu Glu Lys Val
 85          90          95
Arg Arg Ile Ser Glu Lys Tyr Gly Tyr Tyr Arg Gly Ile Asp Ala Gln
 100          105          110
Glu Phe Asn Met Val Ser Asp Tyr Tyr Thr Phe Ser Asn Tyr Asn Gln
 115          120          125
Leu Lys Tyr Phe Val Asp Ile Ala Arg Lys Ile Glu Arg Leu Ser Pro
 130          135          140
Lys Ala Trp Tyr Leu Gln Ala Ala Asn Pro Val Phe Glu Gly Thr Thr
 145          150          155          160
Leu Val Thr Arg Thr Val Pro Ile Lys Ala Val Gly Phe Cys His Gly
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His Tyr Gly Val Met Glu Ile Val Glu Lys Leu Gly Leu Glu Asn
 180          185          190
Arg Val Asp Trp Gln Val Ala Gly Val Asn His Gly Ile Trp Leu Asn
 195          200          205
Arg Phe Arg Tyr Asn Gly Glu Asp Ala Tyr Pro Leu Leu Asp Arg Trp
 210          215          220
Ile Ser Glu Lys Ser Lys Asp Trp Lys Pro Glu Asn Pro Phe Asn Asp
 225          230          235          240
Gln Leu Ser Pro Ala Ala Ile Asp Met Tyr Arg Phe Tyr Gly Val Met
 245          250          255
Pro Ile Gly Asp Thr Val Arg Asn Ser Ser Trp Arg Tyr His Arg Asp
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Leu Glu Thr Lys Lys Lys Trp Tyr Gly Glu Pro Trp Gly Gly Ala Asp
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Ser Glu Ile Gly Trp Lys Trp Tyr Gln Asp Thr Leu Gly Lys Val Thr
 290          295          300
Glu Ile Thr Lys Lys Val Ala Lys Phe Ile Lys Glu Asn Pro Ser Ala
 305          310          315          320
Arg Leu Ser Asp Leu Gly Ser Val Leu Gly Lys Asp Leu Ser Glu Lys
 325          330          335
Gln Phe Val Leu Glu Val Glu Lys Ile Leu Asp Pro Glu Lys Lys Ser
 340          345          350
Gly Glu Gln His Ile Pro Phe Ile Asp Ala Leu Leu Asn Asp Asn Arg
 355          360          365

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PC Ser Arg Phe Val Ile Asn Ile Pro Asn Lys Gly Ile Ile Gln Gly Ile
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 Asp Asp Asp Val Val Val Glu Val Pro Ala Val Val Asp Arg Asp Gly
 385 390 395 400
 Ile His Pro Glu Lys Ile Ala Pro Pro Leu Pro Glu Arg Val Val Lys
 405 410 415
 Tyr Tyr Leu Arg Pro Arg Ile Met Arg Met Glu Met Ala Leu Glu Ala
 420 425 430
 Phe Leu Thr Gly Asp Ile Arg Ile Ile Lys Glu Val Leu Tyr Arg Asp
 435 440 445
 Pro Arg Thr Lys Ser Asp Glu Gln Val Glu Lys Val Ile Glu Glu Ile
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 Leu Ser Leu Pro Glu Asn Glu Glu Met Arg Lys Asn Tyr Leu Lys Lys
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 <211> 1686
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

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 aaaaagctcg gggtagatgt tctgtggcta acgccaattt ataaatcacc gcagcgggat 180
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 ccgtaccgag atttttatat ttggaaagat caaaaagaag atggaagtgc tccgacgaat 420
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<210> 24
 <211> 561
 <212> PRT
 <213> Unknown

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<400> 24

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 35 40 45
 Trp Leu Thr Pro Ile Tyr Lys Ser Pro Gln Arg Asp Asn Gly Tyr Asp
 50 55 60
 Ile Ser Asp Tyr Phe Val Ile Gln Glu Glu Tyr Gly Thr Met Glu Asp
 65 70 75 80
 Phe Asp Leu Leu Val Thr Glu Ala His Lys Arg Gly Leu Lys Val Ile
 85 90 95
 Met Asp Ile Val Val Asn His Thr Ser Thr Glu His Glu Trp Phe Gln
 100 105 110
 Glu Ala Lys Lys Ser Lys Asp Asn Pro Tyr Arg Asp Phe Tyr Ile Trp
 115 120 125
 Lys Asp Gln Lys Glu Asp Gly Ser Ala Pro Thr Asn Trp Val Ser Lys
 130 135 140
 Phe Gly Gly Ser Ala Trp Glu His Asp Asn Leu Thr Glu Gln Ser Tyr
 145 150 155 160
 Leu His Leu Phe Asp Val Thr Gln Ala Asp Leu Asn Trp Glu Asn Glu
 165 170 175
 Arg Val Arg Arg Ser Val Tyr Asp Met Met Thr Phe Trp Phe Glu Lys
 180 185 190
 Gly Val Asp Gly Phe Arg Leu Asp Val Ile Asn Leu Ile Ser Lys Asp
 195 200 205
 Gln Arg Phe Leu Asp Asp Asp Gly Ser Val Ala Pro Gly Asp Gly Arg
 210 215 220
 Lys Phe Tyr Thr Asp Gly Pro Arg Val His Glu Tyr Met Arg Glu Met
 225 230 235 240
 Asn Gln Glu Val Phe Ser Lys Tyr Asp Ser Met Thr Val Gly Glu Met
 245 250 255
 Ser Ser Thr Thr Val Asp His Cys Ile Gln Tyr Ser His Pro Asp Arg
 260 265 270
 Arg Glu Leu Ser Met Thr Phe Asn Phe His His Leu Lys Val Asp Tyr
 275 280 285
 Pro Asn Gly Glu Lys Trp Ala Leu Ala Asp Phe Asp Phe Ile Lys Leu
 290 295 300
 Lys Glu Ile Leu Ser Thr Trp Gln Thr Glu Met Asn Lys Gly Gly Gly
 305 310 315 320
 Trp Asn Ala Leu Phe Trp Cys Asn His Asp Gln Pro Arg Val Val Ser
 325 330 335
 Arg Tyr Gly Asp Asp Glu Leu Tyr His Asn Lys Ser Ala Lys Met Leu
 340 345 350
 Ala Thr Thr Ile His Leu Met Gln Gly Thr Pro Tyr Ile Tyr Gln Gly
 355 360 365
 Glu Glu Ile Gly Met Thr Asn Pro Lys Phe Ser Ser Ile Asp Glu Tyr
 370 375 380
 Arg Asp Val Glu Ser Leu Asn Val Tyr Glu Ile Lys Arg Ala Gln Gly
 385 390 395 400
 Met Asp Glu Asn Glu Ile Leu Glu Ile Leu Lys His Lys Ser Arg Asp
 405 410 415
 Asn Ser Arg Thr Pro Val Gln Trp Asn Asp Lys Pro Asn Ala Gly Phe
 420 425 430
 Thr Lys Gly Lys Pro Trp Ile His Pro Ala Asp Asn Tyr Arg Lys Ile
 435 440 445
 Asn Val Glu Lys Ala Leu Glu Asp Lys Asp Ser Ile Phe Tyr Phe Tyr
 450 455 460
 Gln Lys Leu Ile Ala Leu Arg Lys Gln Tyr Glu Ile Ile Thr Tyr Gly
 465 470 475 480
 Asn Tyr Glu Leu Ile Leu Gly Glu Asp Glu Gln Ile Phe Ala Tyr Ile
 485 490 495
 Arg Asn Gly Ala Asp Glu Lys Leu Leu Val Ile Asn Asn Phe Tyr Gly
 500 505 510

P	C	Ser	Glu	Thr	Ala	Phe	Glu	Leu	Pro	Glu	Asp	Leu	Thr	Phe	Glu	Gly	Tyr
			515						520						525		
His	Ser	Glu	Ile	Leu	Leu	Ser	Asn	Tyr	Glu	Asp	Ser	Pro	Lys	Glu	Phe		
		530				535					540						
Lys	Arg	Val	Leu	Leu	Arg	Pro	Tyr	Glu	Ser	Ile	Val	Tyr	His	Leu	Lys		
545					550					555					560		
Lys																	